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SEARCH REQUEST FORM

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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: <u>08-15-02</u>	Search Site	Vendors
Searcher: <u>Berkeley</u>	<input checked="" type="checkbox"/> STIC	<input checked="" type="checkbox"/> IG
Terminal time: <u>2.2</u>	<input type="checkbox"/> CM-1	<input checked="" type="checkbox"/> STN
Elapsed time: _____	<input type="checkbox"/> Pre-S	<input checked="" type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input checked="" type="checkbox"/> AFS
Total time: <u>3.5</u>	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: <u>2</u>	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>CGN</u>

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Parkin
09/605573

09/605573

~~FILE~~ 'REGISTRY' ENTERED AT 15:39:41 ON 15 AUG 2002
L1 1 S GRETLMQDQQRLNSWGCKGRIICYTSARWH/SQSP

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS
RN 275801-53-1 REGISTRY
CN 135: PN: JP2000157268 SEQID: 69 unclaimed sequence (9CI) (CA INDEX
NAME)
SQL 30

SEQ 1 GRETLMQDQQ RLNSWGCKGR IICYTSARWH
=====

HITS AT: 1-30

REFERENCE 1: 133:55969

~~FILE~~ 'HCAPLUS' ENTERED AT 15:40:58 ON 15 AUG 2002
L2 1 S L1

L2 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:392837 HCAPLUS
DOCUMENT NUMBER: 133:55969
TITLE: Peptide for detection of Group O HIV-1 and use
for diagnosis
INVENTOR(S): Deleys, Robert; Chen, Jan
PATENT ASSIGNEE(S): Ortho-Clinical Diagnostics, Inc., USA
SOURCE: Jpn. Kokai Tokkyo Koho, 103 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 2000157268	A2	20000613	JP 1999-338385	19991129
US 6149910	A	20001121	US 1999-433428	19991104
EP 1013766	A2	20000628	EP 1999-309491	19991129

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.:
US 1998-110292P P 19981130
US 1999-119138P P 19990208
US 1999-433428 A 19991104

AB Disclosed are the peptides derived from the immunodominant region of the Group O HIV-1 gp41 envelope protein, which do not correspond to any known naturally occurring Group O sequence or variant. The peptides bind to the antibodies to Group O HIV-1. The peptides are useful in detecting antibodies arise from the infection by Group O HIV-1. The peptides may be prepd. in a hybrid form with that of Group M HIV-1.

IT 275801-53-1
RL: PRP (Properties)
(unclaimed sequence; peptide for detection of Group O HIV-1 and use for diagnosis)

FILE 'HOME' ENTERED AT 15:41:07 ON 15 AUG 2002

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 10:11:26 ; Search time 30.17 Seconds

(without alignments)
110.448 Million cell updates/sec

Title: US-09-605-573a-69

Perfect score: 173
Sequence: 1 GRETLMOODORLNSMCKGRITCYTSARWH 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

otal number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_032802.*
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT.*
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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	30	21	AA12264
2	157	90.8	35	21	AA12259
3	157	90.8	149	21	AA12262
4	157	90.8	220	21	AA12261
5	157	90.8	368	21	AA12255
6	157	90.8	439	21	AA12252
7	155	89.6	28	21	AA12257
8	134	77.5	23	21	AA12256
9	133	76.9	23	21	AA12254
10	132	76.3	23	21	AA12255
11	131	75.7	33	21	AA12236

12	131	75.7	40	17	AAW07343	Partial sequence o
13	130	75.1	32	19	AAW80469	Peptide derived fr
14	130	75.1	33	21	AA12229	Partial sequence o
15	130	75.1	36	21	AAV67606	Peptide #6 for det
16	130	75.1	113	20	AAV05554	HIV-1 group O isol
17	129	74.6	33	21	AA12231	Partial sequence o
18	129	74.6	40	17	AAW07346	Partial sequence o
19	128	74.0	33	21	AA12208	Partial sequence o
20	128	74.0	33	21	AA12215	Partial sequence o
21	128	74.0	33	21	AA12216	Partial sequence o
22	128	74.0	33	21	AA12218	Partial sequence o
23	128	74.0	33	21	AA12219	Partial sequence o
24	128	74.0	35	15	AA12219	Partial sequence o
25	128	74.0	35	20	AAW93073	HIV-type virus MYP
26	128	74.0	36	20	AAV31617	HIV isolate MYP-51
27	128	74.0	36	21	AAV67607	Peptide #7 for det
28	128	74.0	36	21	AAV55784	HIV gp41 antigen p
29	128	74.0	36	22	AAW62574	Anti-HIV-1 group O
30	128	74.0	167	19	AAW62574	SEQ ID NO. 105 fro
31	128	74.0	204	15	AAV22909	HIV isolate MYP-51
32	128	74.0	351	15	AAV22909	Human Immunodefici
33	128	74.0	351	20	AAV51687	Partial sequence o
34	127	73.4	351	20	AAW93072	Partial sequence o
35	127	73.4	32	22	AAW93072	Partial sequence o
36	127	73.4	33	21	AA12212	Partial sequence o
37	127	73.4	36	20	AAV30515	Peptide #13 for de
38	127	73.4	36	21	AAV97777	Peptide #15 for de
39	127	73.4	36	21	AAV67613	HIV (Group O) Pept
40	127	73.4	36	21	AAV67615	Peptide antigen cr
41	127	73.4	36	22	AAV55786	Partial sequence o
42	127	73.4	36	22	AAW07352	HIV-1 group O isol
43	127	73.4	111	20	AAV05561	Partial sequence o
44	126	72.8	33	21	AA12230	Partial sequence o
45	126	72.8	40	17	AAW07345	Partial sequence o

ALIGNMENTS

RESULT 1
ID AAB12264 standard; peptide: 30 AA.
AC AAB12264;
XX
XX
10-NOV-2000 (first entry)
XX
XX
HIV-1 gp41 immunodominant region consensus sequence peptide 147-5.
DE HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
KW acquired immunodeficiency syndrome; group O HIV; gp41.
RW Human immunodeficiency virus type 1.
OS EPI013766-A2.
XX
XX
28-JUN-2000.
PD
XX
29-NOV-1999; 99EP-0309491.
PF
XX
30-NOV-1998; 98US-0110292.
PR 08-FEB-1999; 99US-0119138.
PR 04-NOV-1999; 99US-0433428.
PA
XX
(ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
PI De Leys R, Zheng J;
XX WPI, 2000-402205/35.
XX
XX New antigenic peptides and peptide functional derivatives, useful for
PT detection of antibodies produced in response to human immunodeficiency
PT virus group O antibodies -

XX PS Claim 1; Page 36; 52pp; English.

XX CC The present sequence is peptide 147-5 from Human Immunodeficiency Virus

CC CC Type 1 (HIV-1). This sequence is a partial consensus sequence of the

CC CC immunodominant region of gp41 protein derived from a variety of HIV-1

CC CC group O (outlier) strains: ANR70, MWP5180, VAV, DUR, POC, FAN, LOB, MAN,

CC CC NAN, ESS, NKO, BCF09, BCF13, BCF14, 686, ABT063, ABT124, ABT123,

CC CC ABT2156, 193Ha, CDC7755, CCI1897, HLD28, 1515, 1516, D47-2d, HCYT2c,

CC CC NR42 and gp41 (see AAB12207 to AAB12236). HIV is the principle

CC CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is

CC CC a HIV envelope protein, and so the present sequence may be used as an

CC CC antigen for the detection of antibodies produced in response to HIV

CC CC infection.

XX SQ Sequence 30 AA;

Query Match 100.0%; Score 173; DB 21; Length 30;

Best Local Similarity 100.0%; Pred. No. 6.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GRETLMODQRLNSWCGKGRITCYTSARWH 30

Db 1 gretlmqdgqrlnswgckgrilcytsarwh 30

RESULT 2

XX ID AAB12259 standard; peptide; 35 AA.

XX AC AAB12259;

XX DT 10-NOV-2000 (first entry)

XX DE Group O HIV-1 gp41 replacement peptide # 1.

XX DE HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;

XX DE acquired immunodeficiency syndrome; group O HIV; gp41.

XX OS Human immunodeficiency virus type 1.

XX PA EPI013766-A2.

XX PD 28-JUN-2000.

XX PF 29-NOV-1999; 99EP-0309491.

XX PR 30-NOV-1998; 98US-0110292.

XX PR 08-FEB-1999; 99US-0119138.

XX PR 04-NOV-1999; 99US-0433428.

XX PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX PI De Leys R, Zheng J;

XX DR WPI: 2000-402205/35.

XX PT New antigenic peptides and peptide functional derivatives, useful for

XX PT detection of antibodies produced in response to human immunodeficiency

XX PT virus group O antibodies -

XX PS Claim 1; Page 37; 52pp; English.

XX CC The present sequence is a group O Human Immunodeficiency Virus Type 1

CC CC (HIV-1) gp41 peptide. HIV is the principle aetiological agent for

CC CC acquired immunodeficiency syndrome (AIDS). gp41 is a HIV envelope

CC CC protein. The present sequence was derived from a sequence homology

CC CC alignment of group O and group M HIV gp41 descending helix sequences.

CC CC The present sequence was used as a group O replacement peptide, where it

CC CC was used to construct mosaic gp41 proteins, in which the group M

CC CC immunodominant region was replaced by the present sequence. The mosaic

CC CC gp41 proteins (AAB12261 and AAB12262) would be useful as antigens, which

CC CC would be used for the detection of anti-group O HIV antibodies produced

CC CC in response to HIV infection.

XX SQ Sequence 35 AA;

Query Match 90.8%; Score 157; DB 21; Length 35;

Best Local Similarity 96.4%; Pred. No. 1.6e-15;

Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMODQRLNSWCGKGRITCYTSARWH 30

Db 8 etlmqngqrlnswgckgrilcytsarwh 35

RESULT 3

XX ID AAB12262 standard; peptide; 149 AA.

XX AC AAB12262;

XX DT 10-NOV-2000 (first entry)

XX DE HIV group M/ group O mosaic protein # 2.

XX DE HIV-1; AIDS; human immunodeficiency virus type 1;

XX DE acquired immunodeficiency syndrome; group O HIV; gp41.

XX OS Human immunodeficiency virus type 1.

XX PA EPI013766-A2.

XX PD 28-JUN-2000.

XX PF 29-NOV-1999; 99EP-0309491.

XX PR 30-NOV-1998; 98US-0110292.

XX PR 08-FEB-1999; 99US-0119138.

XX PR 04-NOV-1999; 99US-0433428.

XX PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX PI De Leys R, Zheng J;

XX DR WPI: 2000-402205/35.

XX PT New antigenic peptides and peptide functional derivatives, useful for

XX PT detection of antibodies produced in response to human immunodeficiency

XX PT virus group O antibodies -

XX PS Claim 15; Page 38-39; 52pp; English.

XX CC Human Immunodeficiency Virus (HIV) is the principle aetiological

CC CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV

CC CC envelope protein, and may be used as an antigen for the detection of

CC CC antibodies produced in response to HIV infection. Mosaic gp41 proteins

CC CC were constructed, in which the immunodominant region of group M HIV was

CC CC replaced by the corresponding region from group O HIV. The mosaic gp41

CC CC proteins would be useful as antigens, used in the detection of anti-group

CC CC O HIV antibodies produced in response to HIV infection. The present

CC CC sequence is one such mosaic protein.

XX SQ Sequence 149 AA;

Query Match 90.8%; Score 157; DB 21; Length 149;

Best Local Similarity 96.4%; Pred. No. 7.5e-15;

Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMODQRLNSWCGKGRITCYTSARWH 30

Db 44 etlmqngqrlnswgckgrilcytsarwh 71


```
RESULT 4
AAB12261
ID AAB12261 standard; peptide: 220 AA.
XX
AC AAB12261;
XX
DT 10-NOV-2000 (first entry)
XX
DE HIV group M/ group O mosaic protein # 1.
XX
KM HIV-1; AIDS: human immunodeficiency virus type 1;
XX acquired immunodeficiency syndrome; group O HIV; gp41.
XX
OS Human immunodeficiency virus type 1.
XX
PN EPI013766-A2.
XX
PD 28-JUN-2000.
XX
PR 29-NOV-1999; 99EP-0309491.
XX
PR 30-NOV-1998; 98US-0110292.
XX 08-FEB-1999; 98US-0119138.
PR 04-NOV-1999; 99US-0433428.
XX
PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
XX
PI De Leys R, Zheng J;
XX
DR WPI: 2000-402205/35.
XX
PT New antigenic peptides and peptide functional derivatives, useful for
XX detection of antibodies produced in response to human immunodeficiency
XX virus group O antibodies -
XX
PS Claim 15; Page 37-38; 52pp; English.
XX
CC Human Immunodeficiency Virus (HIV) is the principle aetiological
XX agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
XX envelope protein, and may be used as an antigen for the detection of
XX antibodies produced in response to HIV infection. Mosaic gp41 proteins
XX were constructed, in which the immunodominant region of group M HIV was
XX replaced by the corresponding region from group O HIV. The mosaic gp41
XX proteins would be useful as antigens, used in the detection of anti-group
XX O HIV antibodies produced in response to HIV infection. The present
XX sequence is one such mosaic protein.
XX
O Sequence 220 AA:

Query Match          90.8%; Score 157; DB 21; Length 220;
Best Local Similarity 96.4%; Pred. No. 1,1e-14;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMODQRLNSWGCKGRITCYTSARWH 30
   |||||:|||||:|||||:|||||:|||||
Db 44 eellmqnqrlnewgckgritcytsarwh 71

RESULT 5
AAB12253
ID AAB12253 standard; peptide: 368 AA.
XX
AC AAB12253;
XX
DT 10-NOV-2000 (first entry)
XX
DE DHFR-hes-MH fusion protein.
XX
KM HIV-1; AIDS: human immunodeficiency virus type 1; DHFR-hes-MH;
XX acquired immunodeficiency syndrome; group O HIV; gp41.
XX
```

```
OS Human immunodeficiency virus type 1.
XX unidentified.
XX
PN EPI013766-A2.
XX
PD 28-JUN-2000.
XX
PR 29-NOV-1999; 99EP-0309491.
XX
PR 30-NOV-1998; 98US-0110292.
XX 08-FEB-1999; 98US-0119138.
PR 04-NOV-1999; 99US-0433428.
XX
PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
XX
PI De Leys R, Zheng J;
XX
DR WPI: 2000-402205/35.
XX
PR New antigenic peptides and peptide functional derivatives, useful for
XX detection of antibodies produced in response to human immunodeficiency
XX virus group O antibodies -
XX
PS Example 5; Fig 6; 52pp; English.
XX
CC Human Immunodeficiency Virus (HIV) is the principle aetiological
XX agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
XX envelope protein, and may be used as an antigen for the detection of
XX antibodies produced in response to HIV infection. Mosaic gp41 proteins
XX were constructed, in which the immunodominant region of group M HIV was
XX replaced by the corresponding region from group O HIV. The mosaic gp41
XX proteins would be useful as antigens, used in the detection of anti-group
XX O HIV antibodies produced in response to HIV infection. The present
XX sequence is a dihydrofolate reductase (DHFR) fusion protein of one such
XX mosaic protein.
XX
SQ Sequence 368 AA:

Query Match          90.8%; Score 157; DB 21; Length 368;
Best Local Similarity 96.4%; Pred. No. 2e-14;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMODQRLNSWGCKGRITCYTSARWH 30
   |||||:|||||:|||||:|||||:|||||
Db 240 eellmqnqrlnewgckgritcytsarwh 267

RESULT 6
AAB12252
ID AAB12252 standard; peptide: 439 AA.
XX
AC AAB12252;
XX
DT 10-NOV-2000 (first entry)
XX
DE DHFR-hENV-MH fusion protein.
XX
KM HIV-1; AIDS: human immunodeficiency virus type 1; DHFR-hENV-MH;
XX acquired immunodeficiency syndrome; group O HIV; gp41.
XX
OS Human immunodeficiency virus type 1.
XX unidentified.
XX
PN EPI013766-A2.
XX
PD 28-JUN-2000.
XX
PR 29-NOV-1999; 99EP-0309491.
XX
PR 30-NOV-1998; 98US-0110292.
XX 08-FEB-1999; 98US-0119138.
PR 04-NOV-1999; 99US-0433428.
XX
```

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 XX De Leys R, Zheng J;
 XX WPI; 2000-402205/35.
 DR
 XX
 PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -
 XX
 PS Example 5; Fig 6; 52pp; English.
 CC
 CC Human Immunodeficiency Virus (HIV) is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. Mosaic gp41 proteins
 CC were constructed, in which the immunodominant region of group M HIV was
 CC replaced by the corresponding region from group O HIV. The mosaic gp41
 CC proteins would be useful as antigens, used in the detection of anti-group
 CC O HIV antibodies produced in response to HIV infection. The present
 CC sequence is a dihydrofolate reductase (DHFR) fusion protein of one such
 CC mosaic protein.
 CC
 SO Sequence 439 AA;
 Query Match 90.8%; Score 157; DB 21; Length 439;
 Best Local Similarity 96.4%; Pred. No. 2.4e-14;
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 3 ETLMQDQRLNSWCGKGRITCYTSARWH 30
 Db 240 etlmqngqrlnswcgkgrilicytsarwh 267
 RESULT 7
 AAB12257
 ID AAB12257 standard; peptide; 28 AA.
 AC AAB12257;
 XX
 DT 10-NOV-2000 (first entry)
 DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 3.
 XX
 KW HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
 KM acquired immunodeficiency syndrome; group O HIV; gp41.
 XX
 XX Human immunodeficiency virus type 1.
 FH Key Location/Qualifiers
 FT MISC-difference 6
 XX /note="Any natural amino acid apart from L-asparagine"
 PN EP1013766-A2.
 PD 28-JUN-2000.
 XX
 PF 29-NOV-1999; 99EP-0309491.
 XX
 PR 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 XX
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 PI De Leys R, Zheng J;
 XX WPI; 2000-402205/35.
 DR
 XX New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency

PT virus group O antibodies -
 XX
 PS Claim 1; Page 36; 52pp; English.
 XX
 CC The present sequence is a peptide 147 related peptide from Human
 CC Immunodeficiency Virus Type 1 (HIV-1). This sequence is a partial
 CC consensus sequence of the immunodominant region of gp41 protein derived
 CC from a variety of HIV-1 group O (outlier) strains: ANT70, WVP5180, VAU,
 CC DUR, POC, FAN, LOB, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686,
 CC ABT063, ABT124, ABT125, ABT126, ABT127, ABT128, 1515,
 CC 1516, D47-2d, HCV72c, N142 and PE41 (see AAB12207 to AAB12236). HIV is
 CC the principle aetiological agent for acquired immunodeficiency syndrome
 CC (AIDS). gp41 is a HIV envelope protein, and so the present sequence may
 CC be used as an antigen for the detection of antibodies produced in
 CC response to HIV infection.
 CC
 SO Sequence 28 AA;
 Query Match 89.6%; Score 155; DB 21; Length 28;
 Best Local Similarity 96.4%; Pred. No. 2.5e-15;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 3 ETLMQDQRLNSWCGKGRITCYTSARWH 30
 Db 1 etlmqngqrlnswcgkgrilicytsarwh 28
 RESULT 8
 AAB12256
 ID AAB12256 standard; peptide; 23 AA.
 AC AAB12256;
 XX
 DT 10-NOV-2000 (first entry)
 DE HIV-1 gp41 immunodominant region consensus sequence peptide 147-4.
 XX
 KW HIV-1; AIDS; human immunodeficiency virus type 1; antibody detection;
 KM acquired immunodeficiency syndrome; group O HIV; gp41.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN EP1013766-A2.
 PD 28-JUN-2000.
 XX
 PF 29-NOV-1999; 99EP-0309491.
 XX
 PR 30-NOV-1998; 98US-0110292.
 PR 08-FEB-1999; 99US-0119138.
 PR 04-NOV-1999; 99US-0433428.
 XX
 PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 PI De Leys R, Zheng J;
 XX WPI; 2000-402205/35.
 DR
 XX New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -
 XX
 PS Claim 1; Page 36; 52pp; English.
 CC
 CC The present sequence is peptide 147-4 from Human Immunodeficiency Virus
 CC Type 1 (HIV-1). This sequence is a partial consensus sequence of the
 CC immunodominant region of gp41 protein derived from a variety of HIV-1
 CC group O (outlier) strains: ANT70, WVP5180, VAU, DUR, POC, FAN, LOB, MAN,
 CC NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABT063, ABT124, ABT125,
 CC ABT126, 193Ha, CDC7755, CDC1897, HLD28, 1515, 1516, D47-2d, HCV72c,
 CC N142 and PE41 (see AAB12207 to AAB12236). HIV is the principle
 CC aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is

CC a HIV envelope protein, and so the present sequence may be used as an
CC antigen for the detection of antibodies produced in response to HIV
CC infection.
XX
XX
SO Sequence 23 AA;

Query Match 77.5%; Score 134; DB 21; Length 23;
Best Local Similarity 95.7%; Pred. No. 2, 1e-12;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 DOORLNSWGCKGRITCYTSARWH 30
Db 1 egqrlnswgckgrilcytsarwh 23

RESULT 9
AAB12254
ID AAB12254 standard; peptide: 23 AA.

XX AAB12254;
DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 1.

KW HIV-1; AIDS: human immunodeficiency virus type 1; antibody detection;
acquired immunodeficiency syndrome; group O HIV; gp41.

OS Human immunodeficiency virus type 1.

XX EPI013766-A2.

XX 28-JUN-2000.

XX 29-NOV-1999; 99EP-0309491.

XX 30-NOV-1998; 98US-0110292.

XX 08-FEB-1999; 99US-0119138.

XX 04-NOV-1999; 99US-0433428.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX De Leys R, Zheng J;

XX WPI; 2000-402205/35.

XX New antigenic peptides and peptide functional derivatives, useful for
XX detection of antibodies produced in response to human immunodeficiency
XX virus group O antibodies -

XX Claim 1; Page 35; 52pp; English.

XX The present sequence is peptide 147 of Human Immunodeficiency Virus Type
XX 1 (HIV-1). This sequence is a partial consensus sequence of the
XX immunodominant region of gp41 protein derived from a variety of HIV-1
XX group O (outlier) strains: ANT70, MYP5180, VAN, DUR, POC, FAN, LOB, MAN,
XX NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686, ABR063, ABR124, ABR123,
XX ABR2156, 193Ha, CDC7755, CDC1897, HUD28, 1515, 1516, D47-2d, HCYT2c,
XX NC42 and PE41 (see AAB12207 to AAB12236). HIV is the principle
XX aetiological agent for acquired immunodeficiency syndrome (AIDS). gp41 is
XX a HIV envelope protein, and so the present sequence may be used as an
XX antigen for the detection of antibodies produced in response to HIV
XX infection.

XX Sequence 23 AA;

OY Query Match 76.9%; Score 133; DB 21; Length 23;
Best Local Similarity 95.7%; Pred. No. 2, 9e-12;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX 8 DOORLNSWGCKGRITCYTSARWH 30

Db. :|||||
1 ngqrlnswgckgrilcytsarwh 23

RESULT 10
AAB12255

ID AAB12255 standard; peptide: 23 AA.

XX AAB12255;

DT 10-NOV-2000 (first entry)

DE HIV-1 gp41 immunodominant region consensus sequence peptide 147 # 2.

KW HIV-1; AIDS: human immunodeficiency virus type 1; antibody detection;
acquired immunodeficiency syndrome; group O HIV; gp41.

OS Human immunodeficiency virus type 1.

XX Key Location/Qualifiers

XX MISC-difference 1 /note="any natural amino acid apart from L-asparagine"

XX EPI013766-A2.

XX 28-JUN-2000.

XX 29-NOV-1999; 99EP-0309491.

XX 30-NOV-1998; 98US-0110292.

XX 08-FEB-1999; 99US-0119138.

XX 04-NOV-1999; 99US-0433428.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX De Leys R, Zheng J;

XX WPI; 2000-402205/35.

XX New antigenic peptides and peptide functional derivatives, useful for
XX detection of antibodies produced in response to human immunodeficiency
XX virus group O antibodies -

XX Claim 1; Page 35; 52pp; English.

XX The present sequence is a peptide 147 related peptide from Human
XX immunodeficiency virus type 1 (HIV-1). This sequence is a partial
XX consensus sequence of the immunodominant region of gp41 protein derived
XX from a variety of HIV-1 group O (outlier) strains: ANT70, MYP5180, VAN,
XX DUR, POC, FAN, LOB, MAN, NAN, ESS, NKO, BCF09, BCF12, BCF13, BCF14, 686,
XX ABR063, ABR124, ABR123, ABR2156, 193Ha, CDC7755, CDC1897, HUD28, 1515,
XX 1516, D47-2d, HCYT2c, NC42 and PE41 (see AAB12207 to AAB12236). HIV is
XX the principle aetiological agent for acquired immunodeficiency syndrome
XX (AIDS). gp41 is a HIV envelope protein, and so the present sequence may
XX be used as an antigen for the detection of antibodies produced in
XX response to HIV infection.

XX Sequence 23 AA;

OY Query Match 76.3%; Score 132; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 DOORLNSWGCKGRITCYTSARWH 30
Db 2 gqrlnswgckgrilcytsarwh 23

RESULT 11
AAB12236
ID AAB12236 standard; peptide: 33 AA.
XX

PA (SNFI) PASTEUR SANOFI DIAGNOSTICS SA.
 XX
 PI Cheneboux DMB, Delagneau JFH, Gadelie SIX, Rieunier FY;
 XX
 DR WPI: 1998-583190/49.
 XX
 XX New synthetic peptide(s) - useful for, e.g. detecting infection by
 PT human immune deficiency virus of group O
 XX
 PS Claim 6; Page 44; 55pp; French.
 XX
 CC AAM80459-74 represent synthetic peptides (either linear or cyclised by
 CC Cys-Cys disulphide bonds). The peptides represent variable sequences
 CC connected around short highly conserved sequences present in isolates
 CC of group O human immune deficiency virus (HIV). The peptides are
 CC useful as immunological reagents for detecting infection by group O
 CC human immune deficiency virus (HIV).
 XX
 SO Sequence 32 AA;

Query Match 75.1%; Score 130; DB 19; Length 32;
 Best Local Similarity 71.4%; Pred. No. 1,1e-11;
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSGCGRICTTSARWH 30
 |||||:|||||:|||||:|||||:|
 DB 3 ecllmgqllnswgcrgrlvcysvkw 30

RESULT 14

AAB12229
 ID AAB12229 standard; peptide: 33 AA.
 XX

AC AAB12229;
 XX

DT 10-NOV-2000 (first entry)
 XX

DE Partial sequence of HIV-1 strain HLD28 gp41 immunodominant region.
 XX

KW HIV-1; AIDS; human immunodeficiency virus type 1; immunodominant region;
 KM acquired immunodeficiency syndrome; group O HIV; gp41; HLD28.
 XX

OS Human immunodeficiency virus type 1.
 XX

PN EP1013766-A2.
 XX

PD 28-JUN-2000.
 XX

PF 29-NOV-1999; 99EP-0309491.
 XX

PR 30-NOV-1998; 98US-0110292.
 XX

PR 08-FEB-1999; 99US-0119136.
 XX

PR 04-NOV-1999; 99US-0433428.
 XX

PA (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.
 XX

PI De Leys R, Zheng J;
 XX

DR WPI: 2000-402205/35.
 XX

PT New antigenic peptides and peptide functional derivatives, useful for
 PT detection of antibodies produced in response to human immunodeficiency
 PT virus group O antibodies -
 XX

PS Example 1; Fig 1; 52pp; English.
 XX

CC The present sequence is a partial gp41 protein of Human Immunodeficiency
 CC virus type 1 (HIV-1) strain HLD28. HIV is the principle aetiological
 CC agent for acquired immunodeficiency syndrome (AIDS). gp41 is a HIV
 CC envelope protein, and may be used as an antigen for the detection of
 CC antibodies produced in response to HIV infection. HLD28 is a member of
 CC HIV group O (outlier). The present sequence is the immunodominant region

CC of gp41. This sequence was used in a sequence homology alignment.
 CC which in turn was used to derive a consensus sequence peptide: peptide
 CC 147 (AAB12254).
 XX

SO Sequence 33 AA;

Query Match 75.1%; Score 130; DB 21; Length 33;
 Best Local Similarity 75.0%; Pred. No. 1,1e-11;
 Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSGCGRICTTSARWH 30
 |||||:|||||:|||||:|||||:|
 DB 6 ecllmgqllnswgcrgrlvcysvkw 33

RESULT 15

AAV67606
 ID AAV67606 standard; peptide: 36 AA.
 XX

AC AAV67606;
 XX

DT 23-MAR-2000 (first entry)
 XX

DE Peptide #6 for detecting HIV-1 group O infection.
 XX

KW Human immunodeficiency virus-1; HIV-1; gp41 envelope protein; detection;
 KM Increased structural stability; diagnostic antigen.
 XX

OS Synthetic.
 XX

PN WO962945-A2.
 XX

PD 09-DEC-1999.
 XX

PF 04-JUN-1999; 99WO-US12446.
 XX

PR 05-JUN-1998; 98US-0088229.
 XX

PR 01-SEP-1998; 98US-0098705.
 XX

PR 15-SEP-1998; 98US-0100422.
 XX

PR 28-JAN-1999; 99WO-US01726.
 XX

PA (PEPT-) PEPTIDE SOLUTIONS INC.
 XX

PI Chowdhury MA, Bernstein D, Mosenbocker MA;
 XX

DR WPI: 2000-086953/07.
 XX

PT Improving properties of peptides for use as diagnostic antigens or for
 PT preventing or treating infections -
 XX

PS Claim 18; Page 61; 83pp; English.
 XX

CC This peptide is derived from the human immunodeficiency virus (HIV)-1
 CC gp41 envelope protein, and is useful for detecting HIV-1 group O
 CC infection. The invention relates to peptides derived from HIV-1 which
 CC have been modified for use as diagnostic antigens in the treatment or
 CC prevention of infection. The structural stability of the peptides can be
 CC increased in four different ways: through the replacement of a
 CC hydrophobic amino acid with a less hydrophobic amino acid; through an
 CC increase in the amount of secondary structure (i.e. alpha helix) in the
 CC peptide; through the removal of a positive charge from the peptide; or
 CC through the constraint of the epitopic sequence via the formation of a
 CC covalent crosslink. Modified peptides of the invention are used to detect
 CC infectious agents specifically HIV-1. Other detectable agents include
 CC Group O viruses; human T-cell lymphotropic virus-T or -II; hepatitis C
 CC and the causative agent of syphilis. The peptides can be used for
 CC prevention or treatment of infections (e.g. as vaccines), or where
 CC expressed from a transgene). More generally almost any peptide can be
 CC similarly modified, e.g. cytokines and interferons; major
 CC histocompatibility complex antigens; hormones; growth factors; tumour
 CC markers or suppressors, or antigens from many other pathogens.

SQ Sequence 36 AA;

Query Match 75.1%; Score 130; DB 21; Length 36;

Best Local Similarity 75.0%; Pred. No. 1.3e-11;

Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 EFLMODQORLNSWGCKGRICYSARWH 30

Db 8 etliqngqrlnlwgcgkgrilicytclskwn 35

Search completed: August 15, 2002, 10:46:04
job time: 2078 sec

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OM protein - protein search, using sw model

Run on:

August 15, 2002, 10:37:56 ; Search time 13.14 Seconds
(without alignments)
55.766 Million cell updates/sec

Title:
US-09-605-573A-69

Sequence:

1 GRETLMODQORLNSWGCKGRITCYTSARWH 30

Scoring table:

BLOSUM62
Gap 10.0, Gapext 0.5

Searched:

231628 seqs, 24425594 residues

Optimal number of hits satisfying chosen parameters:

231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/p/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/p/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/p/ptodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/p/ptodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/p/ptodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/p/ptodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	100.0	30	US-09-433-428D-69	Sequence 69, Appl
2	166	96.0	30	US-09-433-428D-63	Sequence 63, Appl
3	157	90.8	149	US-09-433-428D-67	Sequence 67, Appl
4	157	90.8	220	US-09-433-428D-66	Sequence 66, Appl
5	157	90.8	368	US-09-433-428D-58	Sequence 58, Appl
6	157	90.8	439	US-09-433-428D-57	Sequence 57, Appl
7	155	89.6	28	US-09-433-428D-64	Sequence 64, Appl
8	155	89.6	35	US-09-433-428D-61	Sequence 61, Appl
9	134	77.5	23	US-09-433-428D-59	Sequence 59, Appl
10	133	76.3	23	US-09-433-428D-60	Sequence 60, Appl
11	131	75.7	40	US-09-433-428D-30	Sequence 30, Appl
12	131	75.7	40	US-08-894-699-36	Sequence 36, Appl
13	131	75.7	40	US-09-433-428D-23	Sequence 23, Appl
14	131	75.7	40	US-09-433-428D-25	Sequence 25, Appl
15	130	74.6	33	US-08-894-699-39	Sequence 39, Appl
16	129	74.6	40	US-09-433-428D-2	Sequence 2, Appl
17	129	74.6	33	US-09-433-428D-9	Sequence 9, Appl
18	128	74.0	33	US-09-433-428D-10	Sequence 10, Appl
19	128	74.0	33	US-09-433-428D-12	Sequence 12, Appl
20	128	74.0	33	US-09-433-428D-13	Sequence 13, Appl
21	128	74.0	33	US-08-470-202-62	Sequence 62, Appl
22	128	74.0	35	US-08-471-770-62	Sequence 62, Appl
23	128	74.0	35	US-08-468-059-62	Sequence 62, Appl
24	128	74.0	35	US-09-109-916-62	Sequence 62, Appl
25	128	74.0	4	US-09-109-916-62	Sequence 62, Appl
26	128	74.0	4	US-09-109-916-62	Sequence 62, Appl
27	128	74.0	4	US-09-109-916-62	Sequence 62, Appl

ALIGNMENTS

28	128	74.0	146	2	US-08-394-021-10	Sequence 10, Appl
29	128	74.0	146	4	US-09-131-551-10	Sequence 10, Appl
30	128	74.0	204	4	US-08-965-056-105	Sequence 105, Appl
31	128	74.0	351	1	US-08-470-202-46	Sequence 46, Appl
32	128	74.0	351	1	US-08-471-770-46	Sequence 46, Appl
33	128	74.0	351	2	US-08-468-059-46	Sequence 46, Appl
34	128	74.0	351	4	US-09-109-916-46	Sequence 46, Appl
35	127	73.4	33	4	US-09-433-428D-6	Sequence 6, Appl
36	127	73.4	40	3	US-08-894-699-68	Sequence 68, Appl
37	127	73.4	40	4	US-09-444-410-68	Sequence 68, Appl
38	126	72.8	33	4	US-08-894-699-38	Sequence 38, Appl
39	126	72.8	40	3	US-09-433-428D-24	Sequence 24, Appl
40	126	72.8	40	4	US-08-894-699-41	Sequence 41, Appl
41	125	72.3	33	4	US-09-433-428D-20	Sequence 20, Appl
42	125	72.3	40	3	US-08-894-699-41	Sequence 41, Appl
43	125	72.3	356	1	US-08-602-713-12	Sequence 12, Appl
44	125	72.3	356	4	US-08-989-493-12	Sequence 12, Appl
45	125	72.3	356	4	US-08-989-493-12	Sequence 12, Appl

RESULT 1
US-09-433-428D-69
Sequence 69, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 69
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus
US-09-433-428D-69

Query Match 100.0%; Score 173; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2, 2e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRETLMODQORLNSWGCKGRITCYTSARWH 30
DB 1 GRETLMODQORLNSWGCKGRITCYTSARWH 30

RESULT 2
US-09-433-428D-63
Sequence 63, Application US/09433428D
Patent No. 6149910
GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

NAME/KEY: Xaa is any amino acid
LOCATION: 8
OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-63

Query Match 96.0%; Score 166; DB 4; Length 30;
Best Local Similarity 96.7%; Pred. No. 2.4e-18;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GRETLMODQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
Db 1 GRETLMQXOQRLNSWGCKGRITCYTSARWH 30

RESULT 3
US-09-433-428D-67
Sequence 67, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 67

LENGTH: 149

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-67

Query Match 90.8%; Score 157; DB 4; Length 149;
Best Local Similarity 96.4%; Pred. No. 3.1e-16;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMQDOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
Db 44 ETLMQOQRLNSWGCKGRITCYTSARWH 71

SUIT 4
-09-433-428D-66
Sequence 66, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 66

LENGTH: 220

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-66

Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 ETLMQDOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
Db 44 ETLMQOQRLNSWGCKGRITCYTSARWH 71

RESULT 5
US-09-433-428D-58
Sequence 58, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58

LENGTH: 368

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-58

Query Match 90.8%; Score 157; DB 4; Length 368;
Best Local Similarity 96.4%; Pred. No. 8.5e-16;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMQDOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
Db 240 ETLMQOQRLNSWGCKGRITCYTSARWH 267

RESULT 6
US-09-433-428D-57
Sequence 57, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.

TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O

FILE REFERENCE: CDS-207

CURRENT APPLICATION NUMBER: US/09/433,428D

CURRENT FILING DATE: 1999-11-04

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 57

LENGTH: 439

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:HIV Consensus

OTHER INFORMATION: Sequence

US-09-433-428D-57

Query Match 90.8%; Score 157; DB 4; Length 439;
Best Local Similarity 96.4%; Pred. No. 1e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ETLMQDOQRLNSWGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|||||
Db 240 ETLMQOQRLNSWGCKGRITCYTSARWH 267

RESULT 7
US-09-433-428D-62


```
; Sequence 62, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 62
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 6
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-62
```

```
Query Match          89.6%; Score 155; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 1e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 ETLMDQOORLNSWGCKGRITCYTSARWH 30
DB 1 ETLMOXOORLNSWGCKGRITCYTSARWH 28
```

```
RESULT 8
US-09-433-428D-64
; Sequence 64, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Xaa is any amino acid
; LOCATION: 13
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-64
```

```
Query Match          89.6%; Score 155; DB 4; Length 35;
Best Local Similarity 96.4%; Pred. No. 1.3e-16;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 3 ETLMDQOORLNSWGCKGRITCYTSARWH 30
DB 8 ETLMOXOORLNSWGCKGRITCYTSARWH 35
```

```
RESULT 9
US-09-433-428D-61
; Sequence 61, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
```

```
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 61
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-61
```

```
Query Match          77.5%; Score 134; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.1e-13;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 8 DQORLNSWGCKGRITCYTSARWH 30
DB 1 EQORLNSWGCKGRITCYTSARWH 23
```

```
RESULT 10
US-09-433-428D-59
; Sequence 59, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus
; OTHER INFORMATION: Sequence
; US-09-433-428D-59
```

```
Query Match          76.9%; Score 133; DB 4; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.6e-13;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 8 DQORLNSWGCKGRITCYTSARWH 30
DB 1 NQORLNSWGCKGRITCYTSARWH 23
```

```
RESULT 11
US-09-433-428D-60
; Sequence 60, Application US/09433428D
; Patent No. 6149910
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert J.
; APPLICANT: Zheng, Jian
; TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
; FILE REFERENCE: CDS-207
; CURRENT APPLICATION NUMBER: US/09/433,428D
; CURRENT FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 60
; LENGTH: 23
; TYPE: PRT
```

ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Xaa is any amino acid
LOCATION: 1
OTHER INFORMATION: Description of Artificial Sequence: HIV Consensus
OTHER INFORMATION: Sequence
US-09-433-428D-60

Query Match 76.3%; Score 132; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 2,2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 OORLNSWGCKGRICYSARWH 30
|||||
DB 2 OORLNSWGCKGRICYSARWH 23

RESULT 12

US-09-433-428D-30

Sequence 30, Application US/09433428D
Patent No. 6149910

GENERAL INFORMATION:

APPLICANT: De leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 33
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-433-428D-30

Query Match 75.7%; Score 131; DB 4; Length 33;
Best Local Similarity 75.0%; Pred. No. 4.6e-13;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDOORLNSWGCKGRICYSARWH 30
|||||
DB 6 ETLMDOORLNSWGCKGRICYSARWH 33

RESULT 13

US-08-894-699-36

Sequence 36, Application US/08894699
Patent No. 6030769

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOR
APPLICANT: LOUSSEY-ADAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,699

FILING DATE: 01-DEC-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR96/00294

FILING DATE: 26-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,614

REFERENCE/DOCKET NUMBER: 0354-0020-0PCT

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-894-699-36

Query Match 75.7%; Score 131; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No. 5.7e-13;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMDOORLNSWGCKGRICYSARWH 30
|||||
DB 11 ETLMDOORLNSWGCKGRICYSARWH 38

RESULT 14

US-09-444-410-36

Sequence 36, Application US/09444410
Patent No. 6270975

GENERAL INFORMATION:

APPLICANT: SIMON, FRANCOIS
APPLICANT: SARAGOSTI, SENTOR
APPLICANT: LOUSSEY-ADAKA, IBITISSAM
APPLICANT: LY, THOI-DUONG
APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
TITLE OF INVENTION: VIRUSES, AND USES THEREOF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/444,410

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/894,699

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 95/02236

FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,614
 REFERENCE/DOCKET NUMBER: 0354-0020-OPCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-444-410-36

Query Match 75.7% Score 131; DB 4; Length 40;
 Best Local Similarity 75.0% Pred. No. 5.7e-13;
 Matches 21: Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETLMDODQRLNSWCGCKGRICVTSARWH 30
 |||:|||||:|||||:|||||:|
 Db 11 ETLMDODQRLNSWCGCKGRICVTSARWH 38

RESULT 15
 US-09-433-428D-23
 Sequence 23, Application US/09433428D
 Patent No. 6149910
 GENERAL INFORMATION:
 APPLICANT: De Leys, Robert J.
 APPLICANT: Zheng, Jian
 TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
 FILE REFERENCE: CBS-207
 CURRENT APPLICATION NUMBER: US/09/433,428D
 CURRENT FILING DATE: 1999-11-04
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 23
 LENGTH: 33
 TYPE: PRT
 ORGANISM: Human Immunodeficiency virus type 1
 US-09-433-428D-23

Query Match 75.1% Score 130; DB 4; Length 33;
 Best Local Similarity 75.0% Pred. No. 6.5e-13;
 Matches 21: Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 ETLMDODQRLNSWCGCKGRICVTSARWH 30
 |||:|||||:|||||:|||||:|
 Db 6 ETLMDODQRLNSWCGCKGRICVTSARWH 33

Search completed: August 15, 2002, 10:46:23
 Job time: 507 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 10:41:11 ; Search time 15.15 Seconds

(without alignments)
190.276 Million cell updates/sec

Title: US-09-605-573a-69

Sequence: 1 GRETLMQDQRLNSMGCKGRITCYTSARWH 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR.71:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	68.2	104	2	S52930
2	116	67.1	863	2	A53034
3	114	65.9	877	2	S49197
4	93	53.8	854	1	VCLJST
5	92	53.2	858	1	VCLJG2
6	89	51.4	864	1	VCLJG4
7	88	50.9	357	2	S21990
8	88	50.9	358	2	S22002
9	87	50.3	358	2	S22000
10	87	50.3	358	2	S70417
11	87	50.3	859	1	VCLJST
12	86	49.7	151	2	S30448
13	86	49.7	151	2	S30448
14	86	49.7	151	2	S30452
15	86	49.7	151	2	S30452
16	86	49.7	151	2	S30451
17	86	49.7	856	1	A44963
18	85	49.1	151	2	S30457
19	85	49.1	151	2	S30456
20	85	49.1	151	2	S30455
21	85	49.1	151	2	S30454
22	85	49.1	357	2	S22006
23	85	49.1	357	2	S21994
24	85	49.1	357	2	S22004
25	85	49.1	357	2	S21996
26	85	49.1	358	2	S21992
27	85	49.1	358	2	S21998
28	85	49.1	443	2	C41621
29	85	49.1	445	2	A41621

30	85	49.1	454	2	B41621	env polypeptide D
31	85	49.1	843	1	H44001	env polypeptide pr
32	85	49.1	852	1	VCLJBR	env polypeptide pr
33	85	49.1	852	2	T12016	envelope glycoprote
34	85	49.1	853	2	S54384	envelope polypeptide
35	85	49.1	854	2	S13288	env polypeptide - huma
36	85	49.1	855	1	VCLJ22	env polypeptide pr
37	85	49.1	855	1	VCLJ2R	env polypeptide pr
38	85	49.1	856	1	VCLJH3	env polypeptide pr
39	85	49.1	856	1	VCLJ3W	env polypeptide pr
40	85	49.1	859	1	VCLJ3N	env polypeptide pr
41	85	49.1	859	1	VCLJ3N	env polypeptide pr
42	85	49.1	861	1	VCLJ3C	env polypeptide pr
43	85	49.1	861	1	VCLJ3C	env polypeptide pr
44	85	49.1	868	1	VCLJ34	env polypeptide - huma
45	84	48.6	151	2	S30458	env polypeptide - huma

ALIGNMENTS

RESULT 1
S52930
Gp41 ENV protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
C:Accession: S52930
R:Conen, J.H.M.; Guetard, D.; Philbert, F.; Chamaret, S.; Tabary, T.; Montagnier, L.;
submitted to the EMBL Data Library, January 1995
A:Description: A novel HIV-1 O strain illustrates the diversity of the O group.
A:Reference number: S52929
A:Accession: S52930
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-104 <COH>
A:Cross-references: EMBL:X84328; MID:9695526; PIDN:CA59066.1; PID:9695527
C:Superfamily: type E retrovirus env polypeptide

Query Match 68.2%; Score 118; DB 2; Length 104;
Best Local Similarity 67.9%; Pred. No. 1.2e-09;
Matches 19; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
DB 37 ETLMDQDRLNSMGCKGRITCYTSARWH 64
|||||:|||||:|||||:|||||:|

RESULT 2
A53034
gag polypeptide - human immunodeficiency virus type 1 (strain An70)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: A53034
J:Vandenberg, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groe
J. Virol. 68, 1586-1596, 1994
A:Title: Genomic cloning and complete sequence analysis of a highly divergent African
A:Reference number: A53034; MID:94149849
A:Accession: A53034
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-863 <VAN>
A:Cross-references: GB:L02587
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 67.1%; Score 116; DB 2; Length 863;
Best Local Similarity 60.7%; Pred. No. 1.7e-08;
Matches 17; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
|||||:|||||:|||||:|||||:|

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21990; S70423
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S21990
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332, 'X', 334-357 <STE2>
A:Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:960176
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 50.9%; Score 88; DB 2; Length 357;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
| : : | | | | | | | | | | | : : |
Db 85 ERYLKDQDLGIMGCSGRILCTTAVPWN 112

RESULT 8
S22002
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 3L
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22002; S70418
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S22002
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333, 'X', 335-358 <STE2>
A:Cross-references: EMBL:X61352; NID:960186
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 50.9%; Score 88; DB 2; Length 358;
Matches 14; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
| : : | | | | | | | | | | | : : |
Db 86 ERYLKDQDLGIMGCSGRILCTTAVPWN 113

RESULT 9
S22000
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR
A:Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE2>
A:Cross-references: EMBL:X61351
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 50.3%; Score 87; DB 2; Length 358;
Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
| : : | | | | | | | | | | | : : |
Db 86 ERYLKDQDLGIMGCSGRILCTTAVPWN 113

RESULT 10
S70417
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 3B) (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: patient 3B
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-Aug-1999
C:Accession: S70417
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid
A:Reference number: S70417; MUID:92144209
A:Accession: S70417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STE2>
A:Cross-references: EMBL:X61351; NID:960184; PIDN:CAA43614.1; PID:960185
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 50.3%; Score 87; DB 2; Length 358;
Matches 14; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 3 ETLMDQDRLNSMGCKGRITCYTSARWH 30
| : : | | | | | | | | | | | : : |
Db 86 ERYLKDQDLGIMGCSGRILCTTAVPWN 113

RESULT 11
VCLIST
env polyprotein precursor - human immunodeficiency virus type 2 (isolate ST)
N:Alternate names: coat polyprotein
N:Contents: surface glycoprotein gp120; transmembrane glycoprotein gp41
C:Species: human immunodeficiency virus type 2, HIV-2
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1994
C:Accession: H33943
R: Kumar, P.; Hui, H.; Karpas, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.
J. Virol. 64, 890-901, 1990
A:Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A:Reference number: A33943; MUID:90112662
A:Accession: H33943
A:Molecule type: genomic RNA
A:Residues: 1-859 <KUN>
A:Cross-references: EMBL:M86924
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-859/Product: env polyprotein #status predicted <ENV>
F:20-501/Product: surface glycoprotein gp120 #status predicted <SGC>

Query Match 49.7%; Score 86; DB 2; Length 151;
Best Local Similarity 48.1%; Pred. No. 6.2e-05;
Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 3 ETLMDQDQRLNSWCGCKGRITCTYSARW 29
|::|:||||| |::|: |
Db 28 EKVTKDQDQRLNSWCGCAFRQYCHTTEW 54

Search completed: August 15, 2002, 10:46:45
Job time: 334 sec

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[illegible]

FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .)	(POTENTIAL. .)
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	351	351	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	426	426	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	446	446	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	601	601	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	608	608	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. .)	(POTENTIAL. .)
SQ	SEQUENCE	854 AA;	95803 MW;	2E239AFAD4F2DB93	CRC64;

Query Match	53.8%	Score 93	DB 1	Length 854
Best Local Similarity	50.0%	Pred. No. 2.7e-06		
Matches 14	Conservative	5	Mismatches	9
			Indels	0
			Gaps	0
3	ETLMDDOORLNSWCGCKGRITTCYSAFWH	30		
1				1
574	ERYTDDOIIIGLMGCGSKACVCTTYPWN	601		

FT	CARBOHYD	230	230	N-LINKED	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	233	233	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	264	264	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	270	270	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	281	281	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	302	302	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	358	358	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	364	364	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	391	391	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	440	440	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	455	455	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	603	603	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	612	612	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
FT	CARBOHYD	628	628	N-LINKED <th>(GLCNAC. .)</th> <th>(POTENTIAL).</th>	(GLCNAC. .)	(POTENTIAL).
SO	SEQUENCE	857 AA:	96869 MM:	F881C6755B5746DF	CRC64:	

Query Match

Best Local Similarity 53.8%; Score 93; DB 1; Length 857;

Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 3 ETLMDQDRLNSWCGCKGRITCYTSAW 29

I : : : I I I I I I I : : I I I : I

Db 575 EKVLRDQARLNSWCGCAFROYCYTIVLM 601

RESULT	2			
ENV_HV2KR				
ID	ENV_HV2KR	STANDARD:	PRT:	857 AA.
DC	O7A126;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GPI20); Transmembrane glycoprotein (GPI1)].			
GN	ENV			
OS	Human immunodeficiency virus type 2 (isolate KR) (HIV-2).			
OX	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
RN	NCHI_TaxID=73484;			
RP	(1)			
RA	SEQUENCE FROM N.A.			
RA	Kraus G.K., Talbott R., Leavitt M., Luzznick L., Schmidt A., Badel P., Bartz C., Morton W., Wong-Staal F., Looney D.V.; Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.			
RU				
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CC				
CC	EMBL: U22047; AAA64582.1; InterPro: IPR000328; Env_GP41. InterPro: IPR000777; GP120. Pfam: PF00516; GP120; 1. Pfam: PF00517; GP41; 1.			
DR	AIDS; Coat protein; Polypeptin; Glycoprotein; Transmembrane; Signal.			
KW	SIGNAL.			
FT	1	19	POTENTIAL.	
FT	CHAIN	20	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	504	TRANSMEMBRANE GLYCOPROTEIN.	
FT	CARBOHYD	36	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	69	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	78	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	113	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	121	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	134	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	142	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	159	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	186	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	198	N-LINKED (GLCNAC. . .) (POTENTIAL).	

	RESULT	3		
ENV_HVZRO	ID	ENV_HVZRO	STANDARD:	PRT: 858 AA.
AC	P04577:	13-AUG-1987 (Rel. 05, Created)		
DT		13-AUG-1987 (Rel. 05, Last sequence update)		
DT		16-OCT-2001 (Rel. 40, Last annotation update)		
DE		Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.			
OS		Human immunodeficiency virus type 2 (isolate ROD) (HIV-2).		
OC		Viruses; Retroviral viruses; Retroviridae; Lentivirus.		
OX		NCBI_TaxID=11720;		
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=87173056; PubMed=3031510;			
RA	Guyader M., Emerman M., Sonigo P., Clavel F., Montagnier L.,			
RT	Allison M.;			
RL	"genome organization and transactivation of the human immunodeficiency virus type 2.";			
RL	Nature 326:662-663(1987)."			
CC	-----			
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CC	-----			
DR	EMBL: M15390; AAB00770.1; "			
DR	EMBL: X05291; CAA28914.1; "			
DR	PIR: G26262; VCLJG2.			
DR	HIV; M15390; ENV52ROD.			
DR	InterPro: IPR000328; Env.GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KM	AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	17	
FT	CHAIN	18	501	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	502	858	TRANSMEMBRANE GLYCOPROTEIN.
FT	CARBOHYD	34	34	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	67	67	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	76	76	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 312 312 T -> I (IN REF. 1: AAR0770).
 SQ SEQUENCE 858 AA; 98624 MM; C7266AFLF5C5B9A7 CRC64;

Query Match 53.2%; Score 92; DB 1; Length 858;
 Best Local Similarity 55.6%; Pred. No. 3.9e-06;
 Matches 15; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Oy 3 ETLMOQOQLNSWCGCKGRITCYTSARW 29
 Db 583 EKYLDQARLNSWCGCAFRQVCHTTPW 609

RESULT 4
 ENV_STVAT STANDARD: PRT; 865 AA.
 ID ENV_STVAT
 AC P05886;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 EN ENV.
 OS Simian immunodeficiency virus (TVO-1 isolate) (SIV-AGM).
 OC Viruses; Retroviral; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11731;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88232906; PubMed=3374586;
 RA Fukushima M., Miura T., Hasegawa A., Morikawa S., Tsujimoto H., Miki K., Kitamura T., Hayami M.;
 RT "Sequence of simian immunodeficiency virus from African green monkey, a new member of the HIV/SIV group."
 RL Nature 333:457-461(1988).
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
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 CC -----
 CC EMBL: X07805: CAA30663.2: -.
 CC PIR: G30045: VCLG4.

DR HIV: X07805: ENV\$AGMTY.
 DR InterPro: IPR000328: Env_GP41.
 DR InterPro: IPR000777: GP120.
 DR Pfam: PF00516: GP120; 1.
 DR Pfam: PF00517: GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane; signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 536 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 537 865 TRANSMEMBRANE GLYCOPROTEIN.
 FT SITE 770 770 IN-FRAME TERMINATION CODON.
 FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 373 373 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 661 661 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 865 AA; 99024 MM; 6CEP0F09001D6D95 CRC64;

Query Match 51.4%; Score 89; DB 1; Length 865;
 Best Local Similarity 48.1%; Pred. No. 1.1e-05;
 Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Oy 3 ETLMOQOQLNSWCGCKGRITCYTSARW 29
 Db 608 EKYLDQARLNSWCGCAFRQVCHTTPW 634

RESULT 5
 ENV_STVAT STANDARD: PRT; 854 AA.
 ID ENV_STVAT
 AC Q02837;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 EN ENV.
 OS Simian immunodeficiency virus (isolate AGM / clone GRI-1) (SIV-AGM).
 OC Viruses; Retroviral; Retroviridae; Lentivirus.
 OX NCBI_Taxid=31684;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91220680; PubMed=2024476;
 RA Fomsgaard A., Hirsch V.M., Allan J.S., Johnson P.R.;
 RT "A highly divergent proviral DNA clone of SIV from a distinct species of African green monkey."
 RL Virology 182:397-402(1991).
 CC -1- MISCELLANEOUS: THIS IS AN AFRICAN GREEN MONKEY ISOLATE.
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CC -----

DR EMBL; M56437; AAA91928.1; -

DR EMBL; M58410; AAA47591.1; -

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 24

FT CHAIN 25 522

FT -----

FT CARBOHYD 523 854

FT CARBOHYD 35 35

FT CARBOHYD 68 68

FT CARBOHYD 115 115

FT CARBOHYD 136 136

FT CARBOHYD 153 153

FT CARBOHYD 168 168

FT CARBOHYD 182 182

FT CARBOHYD 199 199

FT CARBOHYD 244 244

FT CARBOHYD 255 255

FT CARBOHYD 265 265

FT CARBOHYD 271 271

FT CARBOHYD 283 283

FT CARBOHYD 295 295

FT CARBOHYD 305 305

FT CARBOHYD 355 355

FT CARBOHYD 400 400

FT CARBOHYD 409 409

FT CARBOHYD 458 458

FT CARBOHYD 472 472

FT CARBOHYD 478 478

FT CARBOHYD 623 623

FT CARBOHYD 624 624

FT CARBOHYD 630 630

FT CARBOHYD 646 646

SO SEQUENCE 854 AA; 96855 MW; 5919CA6C9622912F CRC64;

Query Match 50.3%; Score 87; DB 1; Length 854;

Best Local Similarity 48.1%; Pred. No. 2.2e-05;

Matches 13; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

3 ETLMDQDRLNSWGCGRITCYTSARW 29

594 EKYLEDQRLNSWGCAMKQYCHTTPW 620

RESULT 6

ID ENV_HV2N2 STANDARD; PRT; 856 AA.

AC P05883;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 2 (isolate NIH-2) (HIV-2).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11719;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=8830359; PubMed=3261862;

RA Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laue F., Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.;

RT "Genetic variability between isolates of human immunodeficiency virus RT type 2 is comparable to the variability among HIV type 1.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).

CC -----

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CC -----

DR EMBL; J03654; AAB00761.1; -

DR HTV; J03654; ENV52NTH2.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 20

FT CHAIN 21 492

FT CARBOHYD 37 37

FT CARBOHYD 70 70

FT CARBOHYD 79 79

FT CARBOHYD 112 112

FT CARBOHYD 116 116

FT CARBOHYD 128 128

FT CARBOHYD 133 133

FT CARBOHYD 142 142

FT CARBOHYD 182 182

FT CARBOHYD 183 183

FT CARBOHYD 196 196

FT CARBOHYD 228 228

FT CARBOHYD 231 231

FT CARBOHYD 238 238

FT CARBOHYD 262 262

FT CARBOHYD 268 268

FT CARBOHYD 279 279

FT CARBOHYD 290 290

FT CARBOHYD 300 300

FT CARBOHYD 355 355

FT CARBOHYD 390 390

FT CARBOHYD 400 400

FT CARBOHYD 440 440

FT CARBOHYD 457 457

FT CARBOHYD 602 602

FT CARBOHYD 611 611

FT CARBOHYD 627 627

SO SEQUENCE 856 AA; 96665 MW; A938B0A7E2B881D6 CRC64;

Query Match 50.3%; Score 87; DB 1; Length 856;

Best Local Similarity 51.9%; Pred. No. 2.2e-05;

Matches 14; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

3 ETLMDQDRLNSWGCGRITCYTSARW 29

574 EKYIKDQRLNSWGCARQYCHTTPW 600

RESULT 7

ID ENV_HV2SB STANDARD; PRT; 846 AA.

AC P12449;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 2 (isolate SBLITS) (HIV-2).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11718;

FT	CARBOHYD	237	237	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	258	258	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	272	272	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	285	285	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	291	291	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	327	327	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	351	351	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	381	381	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	389	389	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	395	395	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	435	435	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	598	598	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	603	603	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	612	612	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	803	803	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	843 AA;	95648 MW;	C69PDF971C918B71	CRC64;	
Qy	3	ETLMDDQGRILNSGCKRILCYTSARWH	30			
Db	571	ERYLRDQQLGIGWGSCKLCTTVPWN	598			
Query Match		49.18;	Score 85;	DB 1;	Length 843;	
Best Local Similarity		46.48;	Pred. No. 4.4e-05;			
Matches 13;	Conservative		6;	Mismatches	9;	Indels 0;
						Gaps 0
RESULT 10						
ENV_HV1S1						
ID	ENV_HV1S1	STANDARD;	PRT;	847	AA.	
AC	P19550;					
DT	01-FEB-1991 (rel. 17, Created)					
DT	01-FEB-1991 (rel. 17, Last sequence update)					
DT	15-JUL-1999 (rel. 38, Last annotation update)					
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].					
OS	ENV.					
ON	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).					
OX	Viruses; Retroid viruses; Retroviridae; Lentivirus.					
OC	NCBI_TaxID=11691;					
OX	[1]					
RN	SEQUENCE FROM N.A.					
RP	MEDLINE=90347835; PubMed=2384920;					
RX	Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.,					
RA	"Viral determinants of human immunodeficiency virus type 1 T-cell or					
RT	macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";					
RL	J. Virol. 64:4390-4398(1990).					
CC	-----					
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CC	use by non-profit institutions as long as its content is in no way					
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC	-----					
CC	EMBL; M65024; AAA45072.1; .					
DR	HIV; M38428; ENVSSF162.					
DR	InterPro: IPR000328; Env_GP41.					
DR	InterPro: IPR000777; GP120.					
DR	Plam; PF00516; GP41; 1.					
DR	Plam; PF00517; GP41; 1.					
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;					
KW	signal.					
FT	SIGNAL	1	29			
FT	CHAIN	30	502	EXTERIOR MEMBRANE GLYCOPROTEIN.		
FT	CHAIN	503	847	TRANSMEMBRANE GLYCOPROTEIN.		
FT	DISULFID	53	73	BY SIMILARITY.		
FT	DISULFID	118	203	BY SIMILARITY.		

FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96135 MW; 0A901317ED7FEF2AB CRC64;

Query Match 49.1%; Score 85; DB 1; Length 847;
Best Local Similarity 46.4%; Pred. No. 4,4e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 3 ETLMDQDRLNSGCKGRITCYTSARWH 30
1 : : : : : 1 : : : : : 1 : : : : : 1 : : : : :
Db 575 ERYLRDQDLGIGWCSGKRLCTTVPNW 602

RESULT 11
ENV_HY1M2 STANDARD; PRT; 847 AA.
ID ENV_HY1M2
AC P05880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [contains: exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
CN ENV.

OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salehuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HIV-1/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Science 232:1548-1553(1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.

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CC or send an email to license@isb-sib.ch).

DR EMBL: M12507; ARI12990.1; -;
DR HIV: M12507; ENV\$WMJ2.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Polypeptide; Transmembrane;
KW Signal.

KW CHAIN 1. 29
FT CHAIN 30 501
FT CHAIN 53 847
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 215 244
FT DISULFID 225 236
FT DISULFID 293 326
FT DISULFID 372 435
FT DISULFID 379 408
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
FT CARBOHYD 194 194
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 259 259
FT CARBOHYD 273 273
FT CARBOHYD 286 286
FT CARBOHYD 292 292
FT CARBOHYD 327 327
FT CARBOHYD 334 334
FT CARBOHYD 350 350
FT CARBOHYD 356 356
FT CARBOHYD 380 380
FT CARBOHYD 386 386
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 438 438
FT CARBOHYD 438 438
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73AA5BCAE CRC64;

Query Match 49.1%; Score 85; DB 1; Length 847;
Best Local Similarity 46.4%; Pred. No. 4,4e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 3 ETLMDQDRLNSGCKGRITCYTSARWH 30
1 : : : : : 1 : : : : : 1 : : : : : 1 : : : : :
Db 575 ERYLRDQDLGIGWCSGKRLCTTVPNW 602

RESULT 12
ENV_HY1B8 STANDARD; PRT; 851 AA.
ID ENV_HY1B8
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [contains: exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

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CN	ENV.			
OS	Human immunodeficiency virus type 1 (BH isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.			
OX	NCBI_TaxID=11684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85111123; PubMed=2576615;			
RA	Ratner L., Haseltine W., Patarca R., Lyiak K.J., Stancich B.R.,			
RA	Josephs S.F., Dorian E.R., Rafalski J.A., Whitehorn E.A.,			
RA	Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,			
RA	Laltenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,			
RA	Wong-Staal F.;			
RT	"Complete nucleotide sequence of the AIDS virus, HTLV-II.";			
RL	Nature 313:277-284(1985).			
CC	-----			
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CC	non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch)			
DR	EMBL, K02011; AAA44661.1; -. .			
DR	HIV; K02011; ENVSBH.			
DR	GlycoSuiteDB; P04582; -. .			
DR	InterPro; IPR000328; Env_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KM	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KV	Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT		507	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	331	BY SIMILARITY.
FT	DISULFID	378	440	BY SIMILARITY.
FT	DISULFID	385	413	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	230	230	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	241	234	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	241	241	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	262	262	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	276	276	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	301	301	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	386	386	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	443	443	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	606	606	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	611	611	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	620	620	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	632	632	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	669	669	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD	811	811	N-LINKED (GLCNAC. . .) (POTENTIAL.)

SQ	SEQUENCE	851 AA;	96644 MW;	D16A3C90857785F1 CXC64:
Oy	Query Match	Best Local Similarity	49.1%, Score 85; DB 1; Length 851; Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;	
Db	3 ETLMODORLNSMGCKGRILICYTSARMH 30 :: :: : : 579 ERYLDQQLLGIWGCGKRLICTTAPWN 606			
ENV_HV1BN	RESULT_13			
ID	ENV_HV1BN STANDARD: PRT: 852 AA.			
DC	P12488:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-JUL-1989 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein gp160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]. ENV.			
CN	Human immunodeficiency virus type 1 (BR isolate) (HIV-1).			
OS	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11693;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89085613; PubMed=2789516;			
RA	Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.; "Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia."; Virology 168:79-89(1989).			
RT	-I MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT."			
RL				
CC				
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DR	EMBL; M21098; AAA44221.1; -. PIR; A31667; VCLJBR.			
DR	HIV; M21098; ENVSBRVA.			
DR	InterPro: IPR000328; Env GP41.			
DR	InterPro: IPR000777; GP120.			
DR	pfam; PF00516; GP120; 1.			
DR	pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypotein; Glycoproteins; Transmembrane; Signal.			
RW	SIGNAL.			
FT	CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.			
FT	CHAIN 508 852 TRANSMEMBRANE GLYCOPROTEIN.			
FT	DISULFD 54 74 BY SIMILARTY.			
FT	DISULFD 119 205 BY SIMILARTY.			
FT	DISULFD 126 196 BY SIMILARTY.			
FT	DISULFD 131 155 BY SIMILARTY.			
FT	DISULFD 218 247 BY SIMILARTY.			
FT	DISULFD 228 239 BY SIMILARTY.			
FT	DISULFD 296 330 BY SIMILARTY.			
FT	DISULFD 376 439 BY SIMILARTY.			
FT	DISULFD 383 412 BY SIMILARTY.			
FT	CARBOHD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).			

FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 97203 MM; 2BB866345DEC915F CRC64;

Query Match 49.1%; Score 85; DB 1; Length 852;
Best Local Similarity 46.4%; Pred. No. 4.4e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSGCKGRICYSARWH 30
DB 580 ERYLRDQOLGIMGCGKLCITTVPMW 607

RESULT 14
ENV_HV1S3 STANDARD: PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11690;
P [1]
P SEQUENCE FROM N.A.
P MEDLINE=90317906; PubMed=2370688;
P York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
P "Human immunodeficiency virus type 1 cellular host range,
P replication, and cytopathicity are linked to the envelope region of
P the viral genome.";
P J. Virol. 64:4016-4020(1990).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M38427; AAA45067.1; -;
CC HIV: M38427; ENVSSP3.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MM; EET7BB8D23C9910D CRC64;

Query Match 49.1%; Score 85; DB 1; Length 852;
Best Local Similarity 46.4%; Pred. No. 4.4e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 3 ETLMDQORLNSGCKGRICYSARWH 30
DB 580 ERYLRDQOLGIMGCGKLCITTVPMW 607

RESULT 15
ENV_HV1MF STANDARD: PRT; 853 AA.
AC P19551;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11704;
P [1]
P SEQUENCE FROM N.A.
P MEDLINE=90317877; PubMed=1695254;
P Stevenson M., Haggerty S., Lamontea C., Mann A.M., Meier C.,
P Wasik A.;
P "Cloning and characterization of human immunodeficiency virus type 1
P variants diminished in the ability to induce syncytium-independent
P cytolysis.";

Job time: 212 sec

RL J. Virol. 64:3792-3803(1990).

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CC or send an email to license@isb-sib.ch).

DR EMBL: M33943; AAA44850.1; -.
DR HTV; M33943; ENVSMRA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 509
FT DISULFID 510 853
FT DISULFID 54 74
FT DISULFID 119 203
FT DISULFID 126 194
FT DISULFID 131 157
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 329
FT DISULFID 376 443
FT DISULFID 383 416
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 195 195
FT CARBOHYD 232 232
FT CARBOHYD 239 239
FT CARBOHYD 260 260
FT CARBOHYD 274 274
FT CARBOHYD 287 287
FT CARBOHYD 293 293
FT CARBOHYD 299 299
FT CARBOHYD 330 330
FT CARBOHYD 354 354
FT CARBOHYD 384 384
FT CARBOHYD 390 390
FT CARBOHYD 395 395
FT CARBOHYD 404 404
FT CARBOHYD 446 446
FT CARBOHYD 461 461
FT CARBOHYD 609 609
FT CARBOHYD 614 614
FT CARBOHYD 623 623
FT CARBOHYD 635 635
FT CARBOHYD 672 672
FT CARBOHYD 748 748
FT CARBOHYD 814 814
SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 49.1%; Score 85; DB 1; Length 853;
Best local Similarity 46.4%; Pred. No. 4.5e-05;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
OY 3 ETLMOOQRLNSWCGKGRITCYTSARWH 30
I : : : : : I : : : : : I : : : : : I : : : : : I : : : : :
Db 582 ERYIKDOOLIGIWGCGSKGLICTTAVPWN 609

Search completed: August 15, 2002, 10:50:03

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 10:46:26 : Search time 25.26 Seconds

(Without alignments)
205.457 Million cell updates/sec

Title: US-09-605-573a-69

Sequence: 173

1 GRETLMQDQRLNMGCKGRICYSARWH 30

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Minimum number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhcc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_protist:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	133	76.9	161	15	O91EB5
2	133	76.9	524	15	O91ED3
3	132	76.3	179	15	O91EB4
4	132	76.3	195	15	O91EC6
5	132	76.3	576	15	O91EC6
6	131	75.7	219	15	O91EC6
7	130	75.1	114	15	O91EC6
8	129	74.6	216	15	O91EC5
9	129	74.6	219	15	O91EC5
10	128	74.0	120	15	O91EB6
11	128	74.0	134	15	O91EB6
12	128	74.0	134	15	O91EB6
13	128	74.0	143	15	O91EB6
14	128	74.0	143	15	O91EB6
15	127	73.4	876	15	O91EB6
16	127	73.4	105	15	O91EB6
			172	15	O91EB3

17	127	73.4	234	15	O91EC2	O91EC2	human	immun
18	127	73.4	242	15	O91EC1	O91EC1	human	immun
19	126	72.8	125	15	O91H08	O91H08	human	immun
20	126	72.8	130	15	O91H09	O91H09	human	immun
21	126	72.8	216	15	O91EB5	O91EB5	human	immun
22	126	72.8	232	15	O91EB1	O91EB1	human	immun
23	126	72.8	242	15	O91EB0	O91EB0	human	immun
24	126	72.8	243	15	O91EB5	O91EB5	human	immun
25	126	72.8	544	15	O91EB5	O91EB5	human	immun
26	125	72.3	111	15	O40452	O40452	human	immun
27	125	72.3	114	15	O40457	O40457	human	immun
28	125	72.3	114	15	O40472	O40472	human	immun
29	125	72.3	418	15	O91EB8	O91EB8	human	immun
30	125	72.3	224	15	O91EB8	O91EB8	human	immun
31	124	71.7	124	15	O91H07	O91H07	human	immun
32	124	71.7	126	15	O91H07	O91H07	human	immun
33	124	71.7	134	15	O91H07	O91H07	human	immun
34	124	71.7	183	15	O91H07	O91H07	human	immun
35	124	71.7	200	15	O91H07	O91H07	human	immun
36	124	71.7	213	15	O91H07	O91H07	human	immun
37	124	71.7	220	15	O91H07	O91H07	human	immun
38	124	71.7	225	15	O91H07	O91H07	human	immun
39	124	71.7	512	15	O91H07	O91H07	human	immun
40	124	71.7	517	15	O91H07	O91H07	human	immun
41	124	71.7	532	15	O91H07	O91H07	human	immun
42	124	71.7	545	15	O91H07	O91H07	human	immun
43	123	71.1	112	15	O40454	O40454	human	immun
44	123	71.1	114	15	O40458	O40458	human	immun
45	123	71.1	116	15	O40458	O40458	human	immun

ALIGNMENTS

RESULT 1
ID O91EB5 PRELIMINARY; PRT: 161 AA.
AC O91EB5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP RC
RA STRAIN=BCE57;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.",
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ36405; CAB96253.1; -
DR InterPro: IPR000328; Env_GP41.
KW Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 161 161
SQ SEQUENCE 161 AA; 19305 MW; 5E3AP197E1PDEETC CRC64;
Query Match
Best Local Similarity 76.9%; Score 133; DB 15; Length 161;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 3 ETLMDQDQRLNMGCKGRICYSARWH 30
Db 31 ETLMDQDQRLNMGCKGRICYSARWH 58
RESULT 2
O91ED3

RESULT 3 PRELIMINARY; PRT; 524 AA.

ID Q91ED3
AC Q91ED3: PRELIMINARY; PRT; 524 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=BCF57;
RC Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,
RA Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ133074; CAB96235.1; -
DR EMBL: AJ133074; CAB96235.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 524
FT NON_TER 1 524
SO SEQUENCE 524 AA; 59109 MW; C3D9FF1207AE41 CRC64;

Query Match 76.3%; Score 133; DB 15; Length 524;
Best Local Similarity 78.6%; Pred. No. 2.7e-12;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
DB 355 ETLMOOORLNSWGCKGRITCYTSARWH 382

RESULT 3 PRELIMINARY; PRT; 179 AA.

ID Q91EB4
AC Q91EB4: PRELIMINARY; PRT; 179 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=BCF58;
RC Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ236406; CAB96254.1; -
DR EMBL: AJ236406; CAB96254.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 179
FT NON_TER 1 179
SO SEQUENCE 179 AA; 21225 MW; B060634FF1D4531B CRC64;

Query Match 76.3%; Score 132; DB 15; Length 179;
Best Local Similarity 78.6%; Pred. No. 1.2e-12;
Matches 22; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
DB 34 ETLMOOORLNSWGCKGRITCYTSARWH 61

RESULT 4 PRELIMINARY; PRT; 195 AA.

ID Q91EC6
AC Q91EC6: PRELIMINARY; PRT; 195 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=BCF06;
RC Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
RA Philippe M.;
RT "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ236393; CAB96242.1; -
DR EMBL: AJ236393; CAB96242.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 195
FT NON_TER 1 195
SO SEQUENCE 195 AA; 22964 MW; 2A6363CD0C86A85 CRC64;

Query Match 76.3%; Score 132; DB 15; Length 195;
Best Local Similarity 78.6%; Pred. No. 1.3e-12;
Matches 22; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30
DB 35 ETLMOOORLNSWGCKGRITCYTSARWH 62

RESULT 5 PRELIMINARY; PRT; 576 AA.

ID Q91EF1
AC Q91EF1: PRELIMINARY; PRT; 576 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ENV POLYPEPTIDE (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN=BCF06;
RC Roques P., Robertson D., Diamond F., Sousquiere S., Mauciere P.,
RA Deleigne C., Brun-Vezinet F., Dormont D.;
RT "HIV-1 group O phylogenetic analysis of C2-gp41 region."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ133074; CAB96217.1; -
DR EMBL: AJ133074; CAB96217.1; -
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP41; 1.
DR Pfam: PF00517; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 576
FT NON_TER 1 576
SO SEQUENCE 576 AA; 64977 MW; A21509F3C618195D CRC64;

Query Match 76.3%; Score 132; DB 15; Length 576;
Best Local Similarity 78.6%; Pred. No. 4.3e-12;
Matches 22; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 ETLMOOORLNSWGCKGRITCYTSARWH 30

Db 392 ETLIOMQOORLSMCGCKGRITCYTSARWN 419

```

RESULT 6
ID 09IEC8 PRELIMINARY: PRT: 219 AA.
AC 09IEC8:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF02;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ236391; CAB96240.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 25363 MW; 85C2DC5B5F528907 CRC64;

```

Query Match
Best Local Similarity 75.7%; Score 131; DB 15; Length 219;
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLIOMQOORLSMCGCKGRITCYTSARWN 30
Db 48 ETLIOMQOORLSMCGCKGRITCYTSARWN 75

```

RESULT 7
ID 0A0456 PRELIMINARY: PRT: 114 AA.
AC 0A0456:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE ENVELOPE TRANSMEMBRANE GLYCOPROTEIN (FRAGMENT).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
GN NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GROUP O;
RA Bibollet-Ruche F., Ekasa E., Peeters M., Delaporte E.;
  "Molecular characterization of envelope transmembrane glycoprotein of
  14 new human immunodeficiency virus type 1 group O strains from
  different African countries.";
  Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL: Y09772; CA70911.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 13737 MW; 7907F7F5B51FA9D CRC64;

```

Query Match
Best Local Similarity 75.1%; Score 130; DB 15; Length 114;
Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 ETLIOMQOORLSMCGCKGRITCYTSARWN 30
Db 31 ETLIOMQOORLSMCGCKGRITCYTSARWN 58

```

RESULT 8
ID 09IEC5 PRELIMINARY: PRT: 216 AA.
AC 09IEC5:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF07;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ236394; CAB96243.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 25027 MW; 413AE9BBF1B4FC9A CRC64;

```

Query Match
Best Local Similarity 74.6%; Score 129; DB 15; Length 216;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 ETLIOMQOORLSMCGCKGRITCYTSARWN 30
Db 39 ETLIOMQOORLSMCGCKGRITCYTSARWN 66

```

RESULT 9
ID 09IEB6 PRELIMINARY: PRT: 219 AA.
AC 09IEB6:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE GP41 (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCF14;
RA Roques P., Robertson D., Sandrine S., Christel D., Francois S.,
  Philippe M.;
  "Phylogenetic analysis and sub-typing of 47 HIV-1 group O isolates.";
  Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ236404; CAB96252.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 25353 MW; F65829EB01520D91 CRC64;

```

Query Match
Best Local Similarity 74.4%; Score 129; DB 15; Length 219;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```
RT sequences. Hum. Retroviruses 15
AIDS Res. 1998; 15: 1227-1231.
RL EMBL; AF081815; AAD41227.1; -
DR EMBL; AF081815; AAD41227.1; -
DR InterPro; IPR000328; Env_GP41
DR Pfam; PF00517; GP41. 1.
```

KW Transmembrane.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 16331 MW; 15A17063CD3431D CRC64;

Query Match
Best Local Similarity 74.0%; Score 128; DB 15; Length 143;
Matches 21; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY 3 ETLMDQORLNSWCKGRICVTSARWH 30
DB 61 ETLIONQQLNLNMGCKGRICVTSVRWN 88

RESULT 14
OY 079670 PRELIMINARY; PRT: 876 AA.
AC 079670; 01-NOV-1996 (TREMBlrel. 01, Created)
RT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
CN ENVELOPE PROTEIN GP120/GP41.
OS Human Immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94149848; PubMed=8107219;
RA Gurtler L.G., Hauser P.H., Eberle J., von Bruhn A., Knapp S.,
RT Zekeng L., Tsague J.M., Kapteue L.,
RT "A new subtype of human immunodeficiency virus type 1 (MVP-5180) from
RU Cameroon."
RL J. Virol. 68:1581-1585(1994).
DR EMBL: L20571; AAA44864.1; -;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat Protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 876 AA; 99245 MW; A92F868E37522BAB CRC64;

Query Match
Best Local Similarity 71.4%; Score 128; DB 15; Length 876;
Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
OY 3 ETLMDQORLNSWCKGRICVTSARWH 30
DB 596 ETLIONQQLNLNMGCKGRICVTSVRWN 623

RESULT 15
OY 011939 PRELIMINARY; PRT: 105 AA.
AC 011939; 01-JUL-1997 (TREMBlrel. 04, Created)
RT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
CN ENVELOPE GLYCOPROTEIN (FRAGMENT).
OS Human Immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97340911; PubMed=9197385;
RA Brennan C.A., Hackett J. Jr., Zekeng L., Lund J.K., Vallari A.S.,
RA Hickman R.K., Gurtler L., Kapteue L., von Overbeck J., Hampl H.,
RA Devare S.G.;
RT "Sequence of gp120env immunodominant region of HIV type 1 group O from

RT west central Africa."
RL AIDS Res. Hum. Retroviruses 13:901-904(1997).
DR EMBL: U90132; AAB62815.1; -;
DR InterPro: IPR000328; Env_GP41.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 12531 MW; 2D3D6B5BADCA4382 CRC64;

Query Match
Best Local Similarity 73.4%; Score 127; DB 15; Length 105;
Matches 20; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
OY 3 ETLMDQORLNSWCKGRICVTSARWH 30
DB 24 ETLMDQORLNSWCKGRICVTSARWH 51

Search completed: August 15, 2002, 10:49:45
Job time: 199 sec

Thu Aug 15 11:07:55 2002

us-09-605-573a-69.rspt